



RAW SEQUENCE LISTING ERROR REPORT

The Biotechnology Systems Branch of the Scientific and Technical Information Center (STIC) detected errors when processing the following computer readable form:

Application Serial Number:	/0/5/1,94/
Source:	Parlo
Date Processed by STIC:	12/28/04
_	

THE ATTACHED PRINTOUT EXPLAINS DETECTED ERRORS.
PLEASE FORWARD THIS INFORMATION TO THE APPLICANT BY EITHER:

- 1) INCLUDING A COPY OF THIS PRINTOUT IN YOUR NEXT COMMUNICATION TO THE APPLICANT, WITH A NOTICE TO COMPLY or,
- 2) TELEPHONING APPLICANT AND FAXING A COPY OF THIS PRINTOUT, WITH A NOTICE TO COMPLY

FOR CRF SUBMISSION AND PATENTIN SOFTWARE QUESTIONS, PLEASE CONTACT MARK SPENCER, TELEPHONE: 571-272-2510; FAX: 571-273-0221

TO REDUCE ERRORED SEQUENCE LISTINGS, PLEASE USE THE <u>CHECKER</u> <u>VERSION 4.2 PROGRAM</u>, ACCESSIBLE THROUGH THE U.S. PATENT AND TRADEMARK OFFICE WEBSITE. SEE BELOW FOR ADDRESS:

http://www.uspto.gov/web/offices/pac/checker/chkrnote.htm

Applicants submitting genetic sequence information electronically on diskette or CD-Rom should be aware that there is a possibility that the disk/CD-Rom may have been affected by treatment given to all incoming mail. Please consider using alternate methods of submission for the disk/CD-Rom or replacement disk/CD-Rom. Any reply including a sequence listing in electronic form should NOT be sent to the 20231 zip code address for the United States Patent and Trademark Office, and instead should be sent via the following to the indicated addresses:

- 1. EFS-Bio (<http://www.uspto.gov/ebc/efs/downloads/documents.htm>, EFS Submission User Manual ePAVE)
- 2. U.S. Postal Service: Commissioner for Patents, P.O. Box 1450, Alexandria, VA 22313-1450
- 3. Hand Carry, Federal Express, United Parcel Service, or other delivery service (EFFECTIVE 06/05/04):
 U.S. Patent and Trademark Office, 220 20th Street S., Customer Window, Mail Stop Sequence, Crystal Plaza Two, Lobby, Room 1B03, Arlington, VA 22202

Revised 05/17/04

Raw Sequence Listing Error Summary

RROR DETECTED	SUGGESTED CORRECTION SERIAL NUMBER: 10/517,941
TTN: NEW RULES CASES	: PLEASE DISREGARD ENGLISH "ALPHA" HEADERS, WHICH WERE INSERTED BY PTO SOFTWARE
Wrapped Nucleics Wrapped Aminos	The number/text at the end of each line "wrapped" down to the next line. This may occur if your file was retrieved in a word processor after creating it. Please adjust your right margin to .3; this will prevent "wrapping."
2Invalid Line Length	The rules require that a line not exceed 72 characters in length. This includes white spaces.
3Misaligned Amino Numbering	The numbering under each 5 th amino acid is misaligned. Do not use tab codes between numbers; use space characters, instead.
4Non-ASCII	The submitted file was not saved in ASCII(DOS) text, as required by the Sequence Rules. Please ensure your subsequent submission is saved in ASCII text.
5Variable Length	Sequence(s) contain n's or Xaa's representing more than one residue. Per Sequence Rules, each n or Xaa can only represent a single residue. Please present the maximum number of each residue having variable length and indicate in the <220>-<223> section that some may be missing.
6PatentIn 2.0 "bug"	A "bug" in PatentIn version 2.0 has caused the <220>-<223> section to be missing from amino acid sequences(s) Normally, PatentIn would automatically generate this section from the previously coded nucleic acid sequence. Please manually copy the relevant <220>-<223> section to the subsequent amino acid sequence. This applies to the mandatory <220>-<223> sections for Artificial or Unknown sequences.
7Skipped Sequences (OLD RULES)	Sequence(s) missing. If intentional, please insert the following lines for each skipped sequence: (2) INFORMATION FOR SEQ ID NO:X: (insert SEQ ID NO where "X" is shown) (i) SEQUENCE CHARACTERISTICS: (Do not insert any subheadings under this heading) (xi) SEQUENCE DESCRIPTION:SEQ ID NO:X: (insert SEQ ID NO where "X" is shown) This sequence is intentionally skipped
	Please also adjust the "(ii) NUMBER OF SEQUENCES:" response to include the skipped sequences.
8Skipped Sequences (NEW RULES)	Sequence(s) missing. If intentional, please insert the following lines for each skipped sequence. <210> sequence id number <400> sequence id number 000
9Use of n's or Xaa's (NEW RULES)	Use of n's and/or Xaa's have been detected in the Sequence Listing. Per 1.823 of Sequence Rules, use of <220>-<223> is MANDATORY if n's or Xaa's are present. In <220> to <223> section, please explain location of n or Xaa, and which residue n or Xaa represents.
Invalid <213> Response	Per 1.823 of Sequence Rules, the only valid <213> responses are: Unknown, Artificial Sequence, or scientific name (Genus/species). <220>-<223> section is required when <213> response is Unknown or is Artificial Sequence
Use of <220>	Sequence(s) missing the <220> "Feature" and associated numeric identifiers and responses. Use of <220> to <223> is MANDATORY if <213> "Organism" response is "Artificial Sequence" or "Unknown." Please explain source of genetic material in <220> to <223> section. (See "Federal Register," 06/01/1998, Vol. 63, No. 104, pp. 29631-32) (Sec. 1.823 of Sequence Rules)
PatentIn 2.0 "bug"	Please do not use "Copy to Disk" function of PatentIn version 2.0. This causes a corrupted file, resulting in missing mandatory numeric identifiers and responses (as indicated on raw sequence listing). Instead, please use "File Manager" or any other manual means to copy file to floppy disk.
13 Misuse of n/Xaa	"n" can only represent a single nucleotide; "Xaa" can only represent a single amino acid
-	

AMC - Biotechnology Systems Branch - 09/09/2003



PCT

RAW SEQUENCE LISTING DATE: 12/28/2004
PATENT APPLICATION: US/10/517,941 TIME: 11:51:26

```
3 <110> APPLICANT: Crucell Holland B.V.
              Bakker, Alexander B.H.
              Meester-Rood, Pauline M.L.
              Bakker, Adrianus Q.
      8 <120> TITLE OF INVENTION: AGONISTIC BINDING MOLECULES TO THE HUMAN OX40 RECEPTOR
     10 <130> FILE REFERENCE: 0077 WO 00 ORD
C--> 12 <140> CURRENT APPLICATION NUMBER: US/10/517,941
C--> 12 <141> CURRENT FILING DATE: 2004-12-13
     12 <150> PRIOR APPLICATION NUMBER: PCT/NL02/00389
     13 <151> PRIOR FILING DATE: 2002-06-13
     15 <160> NUMBER OF SEQ ID NOS: 54
     17 <170> SOFTWARE: PatentIn version 3.1
     19 <210> SEO ID NO: 1
     20 <211> LENGTH: 769
     21 <212> TYPE: DNA
     22 <213> ORGANISM: Artificial sequence
     24 <220> FEATURE:
     25 <223> OTHER INFORMATION:
                                /scFv SC02008
     27 <220> FEATURE:
     28 <221> NAME/KEY: CDS
     29 <222> LOCATION: (3)..(767)
     30 <223> OTHER INFORMATION:
W--> 33 <400> 1
     34 cc atg gct gag gtg cag ctg gtg gag tct ggg gga ggc ttg gtc cag
          Met Ala Glu Val Gln Leu Val Glu Ser Gly Gly Leu Val Gln
     36
                                               10
                                                                               95
     38 cet gga ggg tee etg aga ete tee tgt gea gee tet gga tte ace ttt
     39 Pro Gly Gly Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe
                                            25
     42 agc aac tac acg atg aac tgg gtc cgc cag gcg ccc ggg aag ggg ctg
                                                                              143
     43 Ser Asn Tyr Thr Met Asn Trp Val Arg Gln Ala Pro Gly Lys Gly Leu
     44
                    35
                                        40
     46 gag tgg gtc tca gct att agt ggt agt ggt agc aca tac tac gca
                                                                              191
     47 Glu Trp Val Ser Ala Ile Ser Gly Ser Gly Gly Ser Thr Tyr Tyr Ala
                                    55
     50 gac tee gtg aag gge egg tte ace ate tee aga gac aat tee aag aac
                                                                              239
     51 Asp Ser Val Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser Lys Asn
                                70
     54 acg ctg tat ctg caa atg aac agc ctg aga gcc gag gac acg gcc gtg
                                                                              287
    55 Thr Leu Tyr Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val
    56 80
                            85
                                                90
                                                                     95
    58 tat tac tgt gcc aaa gac cgc tac tcc cag gtg cac tac gcg ttg gat
                                                                              335
     59 Tyr Tyr Cys Ala Lys Asp Arg Tyr Ser Gln Val His Tyr Ala Leu Asp
```

60					100					105					110		
	tac	taa	aac	cag		acc	cta	ata	acc		ctc	gag	aat	acc		aat	383
				Gln			_										
64	4	_		115	2				120				-	125	•	•	
66	tcc	qqc	qqa	acc	qqq	tct	qqq	act	ggt	acg	agc	gag	ctc	gac	atc	caq	431
				Thr													
68		•	130		•		•	135	•				140	•			
70	atq	acq	caq	tct	cca	qac	tca	ctg	ccc	gtc	acc	cct	gga	gag	ccg	gcc	479
				Ser													
72		145	•			-	150					155	_				
74	tcc	atc	tcc	tgc	agg	tct	agt	cag	agc	ctc	ctg	cat	agt	aat	gga	tac	527
				Cys			_	_									
76	160			_		165				•	170					175	
78	aac	tat	ttg	gat	tgg	tac	ctg	cag	aag	gca	ggg	cag	tct	cca	cag	ctc	575
				Asp													
80		-		_	180	_			_	185	_				190		
82	ctg	atc	tat	ttg	ggt	tct	aat	cgg	gcc	tcc	ggg	gtc	cct	gac	agg	ttc	623
				Leu													
84			_	195	_			_	200		_			205			
86	agt	ggc	agt	gga	tca	ggc	aca	gat	ttt	aca	ctg	aaa	atc	agc	aga	gtg	671
				Gly													
88			210					215					220				
90	gag	gct	gag	gat	gtt	ggg	gtt	tat	tac	tgc	cag	cag	tac	tac	aac	cac	719
91	Glu	Ala	Glu	Asp	Val	Gly	Val	Tyr	Tyr	Cys	Gln	Gln	Tyr	Tyr	Asn	His	
92		225					230					235					
94	ccg	acg	acc	ttc	ggc	cag	ggc	acc	aaa	ctg	gaa	atc	aaa	cgc	gcg	gcc	767
95	Pro	Thr	Thr	Phe	Gly	Gln	Gly	Thr	Lys	Leu	Glu	Ile	Lys	Arg	Ala	Ala	
96	240					245					250					255	
98	gc																769
101	<21	.0> 5	SEQ I	D NO): 2												
102	<21	1> I	LENG	TH: 2	255												•
103	<21	.2> 7	TYPE:	PRT	ľ												0
104	<21	.3> (ORGAI	NISM:	Art	ific	cial	sequ	lence	2		1		•	. //	1	vee?
106	<22	0> I	PEAT	JRE:									1		th	e sol	nee,
107	<22	3> 0	THE	RINE	ORM	OITA	1:/ sc	Fv S	3C020	800) L	UH	، النه	. حدصر	<i>)</i>	•	
109	<40	0 > 5	SEQUE	ENCE:	: 2						_						
	1100	Ala	ı Glı	ı Val	. 011	ı Leı	ı Val	Glu	ı Ser		/ Gl	/ Gly	, Lei	ı Val		n Pro	
112		_			5				_	10		_			15		
															r Phe	e Ser	
				20												_	
		Туз		: Met	: Ası	ı Trp	va]	. Arg	g Glr	ı Ala	Pro	Gly	/ Lys	s Gly	/ Let	ı Glu	
120			35			_		40			_	•	45	_		_	
			. Sei	: Ala	ı Ile	e Sei		, Ser	: Gly	Gl _y	/ Sei		: Tyı	r Tyı	r Ala	a Asp	
124		50	_		_		55		_	_	_	60	_	_	_	_,	
		· Va]	Lys	s Gly	/ Arc		Thi	: Ile	e Ser	Aro	_) Ası	ı Sei	r Lys	s Ası	n Thr	
128		_	_			70	-	_			75 ~3	_				80	
		Туг	: Lei	ı Glr		: Asr	ı Ser	Leu	ı Arg		ı Glu	ı Ası	Thi	r Ala		l Tyr	
132		-		_	85	_	_	_		90		_		_	95	_	
135	Tyr	Cys	s Ala	a Lys	: Asr	Arg	ј Туг	Ser	: GIr	ı Val	His	ту1	: Ala	a Let	ı Ası	Tyr	

Input Set : D:\0077 (OX40).ST25.txt
Output Set: N:\CRF4\12282004\J517941.raw

13	6			100					105					110			
13	9 Trp	Gly	Gln	Gly	Thr	Leu	Val	Thr	Val	Leu	Glu	Glv	Thr	Glv	Glv	Ser	
14			115	2				120				1	125	1	1		
	3 Gly	Glv		G137	Sar	Glv	Thr		Thr	Sar	Glu	Len		Tlo	Gln	Mot	
14		130	1111	Cly	DCI	Cry	135	Gry	1111	SCI	GIU	140	nsp	110	GIII	Mec	
	_		0	D					**- 7	m1			~7	_			
	7 Thr		ser	Pro	Asp		ьeu	Pro	vaı	Thr		GIY	GIU	Pro	Ala		
	8 145					150					155					160	
15	1 Ile	Ser	Cys	Arg	Ser	Ser	Gln	Ser	Leu	Leu	His	Ser	Asn	Gly	Tyr	Asn	
15	2				165					170					175		•
15	5 Tyr	Leu	Asp	Trp	Tyr	Leu	Gln	Lys	Ala	Gly	Gln	Ser	Pro	Gln	Leu	Leu	
15	6			180					185					190		•	
19	9 Ile	Tyr	Leu	Gly	Ser	Asn	Arq	Ala	Ser	Gly	Val	Pro	Asp	Arq	Phe	Ser	
16		•	195	- 1			- 3	200		2			205				
	3 Gly	Ser		Ser	Glv	Thr	Agn		Thr	T.011	Lve	Tla		Ara	V=1	Glu	
16		210	GLY	Der	GLY	1111	_	FIIC	TILL	пец	БУБ		261	Arg	vai	Giu	
			7	17. 7	~ 1	TT_ 7	215			~ 1	~ 1	220	m		***	D	
	7 Ala		Asp	vai	GIY		ıyr	Tyr	Cys	Gin		Tyr	ıyr	Asn	Hls		
	8 225			_		230				_	235			_		240	
17	1 Thr	Thr	Phe	Gly	Gln	Gly	Thr	Lys	Leu	Glu	Ile	Lys	Arg	Ala	Ala		
17	2				245					250					255	-	
17	5 <21	0>. S	EQ II	ои с	: 3												
17	6 <21	1> L	ENGTI	H: 7	75												
17	7 <21	2> T	YPE:	DNA													
	8 <21				Art	ific:	ial s	seaue	ence								
	0 <22									-							
	1 <22				ימשפר	rt (Ni	C 5 6 1	i Par Co	7020	na							
	3 <22				JKIM.	TOIV	. 501		2020	J)						
					ana	Ì					/						
	4 <22					/	\										
	5 <22																
	6 <22		THER	INF	ORMA'	FION:	: ,										
18	9 < 40	0> 3															
19	0 cc	atg 🤉	gct g	gag g	gtg (cag d	ctg g	gtg g	gag t	cct g	ggg 9	gga g	ggc 1	tg g	gtc (cag	47
19	1	Met 1	Ala (Glu V	Val (Gln I	Leu V	Val (Glu S	Ser (Gly (Gly (3ly 1	Leu V	/al (Gln	
19	2	1				5					10				:	15	
	4 cct	qqq	qqq	tcc	cta	aqa	ctc	tcc	tqt	qca	qcc	tct	qqa	ttc	acc	ttc	95
	5 Pro				_	-			_	-	-						
19		1	1		20	3			-, 5	25			- <u>-</u> <u>1</u>		30		
	8 agc	aaa	tac	tat		220	+~~	ata	000		~~~	000	~~~			at~	1/2
																	143
	9 Ser	GIA	TAT		met	ASII	ттЪ	val	_	GIII	ATG	PLO	GTA	_	стХ	Leu	
20				35					40	,				45			
	2 gag																191
20	3 Glu	\mathtt{Trp}	Val	${ t Gly}$	Arg	Thr	Arg	Asn	Lys	Ala	Asn	Ser	Tyr	Thr	Thr	Glu	
20			50					55					60				
20	6 tac	gcc	gcg	tct	gtg	aaa	ggc	aga	ttc	acc	atc	tca	aga	gat	gat	tca	239
20	7 Tyr	Ala	Ala	Ser	Val	Lys	Gly	Arq	Phe	Thr	Ile	Ser	Ara	Āsp	Āsp	Ser	
20		65			•	•	70	ر		- •	_	75	ر	- 1	- 1-	-	
	0 aag		tca	ata	tat	cta	_	ato	aac	act	cta		acc	gag	gac	aca	287
	1 Lys																207
		TOIL	SCI	пец	TAT		GIII	met	Wall	Set		Arg	HIG	GIU	нар		
	2 80	L	.		.	85				4	90			. .		95	~~=
- 71	4 acc	qtq	tat	tac	tgt	gcc	aaa	gac	cgc	tac	gtc	aac	acg	tcg	aac	gcg	335
2 1	- 900																

W-->

215 216	Ala	Val	Tyr	Tyr	Cys 100	Ala	Lys	Asp	Arg	Tyr 105	Val	Asn	Thr	Ser	Asn 110	Ala	
	++-	~~+	+ > 0	+~~		a aa	~~~	200	ata		200	a+a	ata	<i>~~~</i>	-	200	383
													ctc				303
	Pne	Asp	Tyr		GIY	GIN	GIY	ini		vai	THE	vai	Leu		GIY	IIIL	
220		_		115					120					125			
													agc				431
223	Gly	Gly	Ser	Gly	Gly	Thr	Gly	Ser	Gly	Thr	Gly	Thr	Ser	Glu	Leu	Asp	
224			130					135					140				
226	atc	cag	atg	aca	cag	tct	cca	gac	tca	ctg	CCC	gtc	acc	cct	gga	gag	479
227	Ile	Gln	Met	Thr	Gln	Ser	Pro	Asp	Ser	Leu	Pro	Val	Thr	Pro	Gly	Glu	
228		145					150					155					
230	ccg	gcc	tcc	atc	tcc	tgc	aga	tct	agt	cag	agc	ctc	ctg	cat	agt	aat	527
231	Pro	Ala	Ser	Ile	Ser	Cys	Arg	Ser	Ser	Gln	Ser	Leu	Leu	His	Ser	Asn	
232						165					170					175	
234	qqa	tac	aac	tat	ttq	qat	taa	tac	ctq	caq	aaq	cca	ggg	caq	tct	cca	575
					_	_			_	_	-		Gly	_			
236	1	-1-		-1-	180			-2-		185			2		190		
	caq	ata	cta	atc		t.t.a	aat.	tct	aat.		acc	taa	ggg	atc	cct	gac	623
	_		_			_					_		Gly	-			
240	0111			195	-1-		1		200	5			1	205		E	
	add	ttc	agt		agt	gga	tca	aac		gat	+++	aca	ctg		atc	age	671
													Leu				•
244	**** 9	1110	210	OI,	-	OI,	001	215		пор			220	-10			
	202	ata		act	cac	cat	att		att	tat	tac	tac	cag	cad	tac	cca	719
													Gln				,
	Arg	225	GIU	Ala	птъ	птр	230	GIY	vai	ıyı	IYI	235	GIII	GIII	ıyı	FIO	
248			~~~			++-		~~~	~~~	200			~~~	2+4	222	aaa	767
													gaa				/6/
		GTÀ	PIO	PLO	TIIT		GIY	GIII	GIY	IIIL	_	ьец	Glu	116	пÃр	255	
	240					245					250	•				255	775
	_	gcc	gc														//5
	Ala																
)> SI															
		L> LE			o /												
		2> TY			3												
					Art	IIIC:	laı s	seque	ence								
)> FI							~~~	•	\						
						LION:	:\sci	v s	30200)9 /)						
)> SI				_					~	~ 7	_		~-7	_	
		Ala	Glu	Val		Leu	Val	GIu	Ser	-	GLY	GIY.	Leu	Val		Pro	
270					5				_	10		_			15		
	Gly	Gly	Ser	Leu	Arg	Leu	Ser	Cys	Ala	Ala	Ser	Gly	Phe		Phe	Ser	
274				20					25					30			
277	Gly	Tyr	Ser	Met	Asn	Trp	Val	Arg	Gln	Ala	Pro	Gly	Lys	Gly	Leu	Glu	
278			35					40					45				
281	Trp	Val	Gly	Arg	Thr	Arg	Asn	Lys	Ala	Asn	Ser	Tyr	Thr	Thr	Glu	Tyr	
282		50					55					60					
285	Ala	Ala	Ser	Val	Lys	Gly	Arg	Phe	Thr	Ile	Ser	Arg	Asp	Asp	Ser	Lys	
286	65					70					75					80	
		Ser	Leu	Tyr	Leu	Gln	Met	Asn	Ser	Leu	Arg	Ala	Glu	Asp	Thr	Ala	
				_							_						

290					85					90					95			
293	Val	Tyr	Tyr	Cys	Ala	Lys	Asp	Arg	Tyr	Val	As'n	Thr	Ser	Asn	Ala	Phe		
294				100					105					110				
297	Asp	Tyr	Trp	Gly	Gln	Gly	Thr	Leu	Val	Thr	Val	Leu	Glu	Gly	Thr	Gly		-
298			115					120					125					
301	Gly	Ser	Gly	Gly	Thr	Gly	Ser	Gly	Thr	Gly	Thr	Ser	Glu	Leu	Asp	Ile		
302	_	130	_	_		_	135	_				140						
305	Gln	Met	Thr	Gln	Ser	Pro	Asp	Ser	Leu	Pro	Val	Thr	Pro	Gly	Glu	Pro		
306	145					150					155					160		
309	Ala	Ser	Ile	Ser	Cys	Arg	Ser	Ser	Gln	Ser	Leu	Leu	His	Ser	Asn	Gly		
310					165					170					175			
313	Tyr	Asn	Tyr	Leu	Asp	Trp	Tyr	Leu	Gln	Lys	Pro	Gly	Gln	Ser	Pro	Gln		
314				180					185					190				
317	Leu	Leu	Ile	Tyr	Leu	Gly	Ser	Asn	Arg	Ala	Ser	Gly	Val	Pro	Asp	Arg		
318			195					200					205					•
321	Phe	Ser	Gly	Ser	Gly	Ser	Gly	Thr	Asp	Phe	Thr	Leu	Lys	Ile	Ser	Arg		
322		210					215					220				•		
325	Val	Glu	Ala	Hiş	His	Val	Gly	Val	Tyr	Tyr	Cys	Gln	Gln	Tyr	Pro	Leu		
326	225					230				•	235					240		
329	Gly	Pro	Pro	Thr	Phe	Gly	Gln	Gly	Thr	Lys	Leu	Glu	Ile	Lys	Arg	Ala		
330					245					250					255			
333	Ala																	
337	<210	0> SI	EQ II	ON C	: 5													
338	<21	1> LI	ENGT	H: 73	36													
226	-211	2> T	DE.	DNIA													_	
333	<21		LPB.	DIM							•				•			
	<213				Arti	ifici	ial s	seque	ence		•	_	Tim	PO	RIT	ANT		
340		3 > OI	RGAN:	ISM:	Arti	ifici	ial s	seque	ence			-	Tw	PO	RTT	INT		
340 342	<21	3> OI 0> FI	RGAN: EATUI	ISM: RE:			_			10	H	•						oughou t
340 342 343	<21 <22	3> OF 0> FF 3> O	RGAN: EATUI CHER	ISM: RE: INFO			_			10	· >>>	The	types Seque	of er ence I	rors s listing	bown e: . Please	cist thro	oughou t subsequent
340 342 343 345 346	<21: <22: <22: <22: <22:	3 > OI 0 > FI 3 > O' 0 > FI 1 > NA	RGAN: EATUI THER EATUI AME/I	ISM: RE: INFO RE: KEY:	ORMAT	rion	scI			10	·)	The	types Seque	of er ence I	rors s listing	hown e	cist thro	
340 342 343 345 346 347	<213 <220 <223 <220 <223 <223	3 > OF 0 > FF 3 > OT 0 > FF 1 > NA 2 > LO	RGAN: EATUI THER EATUI AME/I	ISM: RE: INFO RE: KEY: ION:	CDS	rion (scI			10	· >>>	The	types Seque	of er ence I	rors s listing	bown e: . Please	cist thro	
340 342 343 345 346 347	<213 <223 <223 <223 <223 <223 <223	3 > OF	RGAN: EATUI THER EATUI AME/I	ISM: RE: INFO RE: KEY: ION:	CDS	rion (scI			10	· >>>	The	types Seque	of er ence I	rors s listing	bown e: . Please	cist thro	
340 343 343 346 346 347	<213 <223 <223 <223 <223 <223 <223 <223	3 > OF	RGAN: EATUR THER EATUR AME / R DCAT: THER	ISM: RE: INFO RE: KEY: ION: INFO	CDS (3)	rion (73 rion:	SCI 34)	Fv SC	20201))	The the sequ	types Seque tence	of er ence I s for e	rors s listing similar	hown er . Please r errors.	cist thro	subsequent
340 343 343 346 346 347	<21: <22: <22: <22: <22: <22: <22: <22:	3 > OH 0 > FI 3 > OT 0 > FI 1 > NA 2 > LO 3 > OT 0 > 5 atg 9	RGANI CHER CHER CATU CHER CHER CHER CHER	ISM: RE: INFO RE: KEY: ION: INFO	CDS (3). ORMAT	rion (73 rion:	sci 34)	y so	20201	ict s		The the sequ	types Seque tence	of ence I s for a	rrors s listing similar	hown en . Please r errors.	cist thro	
340 343 345 345 347 348 351 352	<21: <22: <22: <22: <22: <22: <22: <40: cc a	3 > OH 0 > FI 3 > O' 0 > FI 1 > NA 2 > LO 3 > O' 0 > 5 atg 9	RGANI CHER CHER CATU CHER CHER CHER CHER	ISM: RE: INFO RE: KEY: ION: INFO	CDS (3). ORMAT	rion. (73 rion: cag c	sci 34)	y so	20201	cct g	Gly (The the sequ	types Seque tence	of ence I s for a	rors s listing similar atc o	hown e: . Please r errors. cag	cist thro	subsequent
340 342 343 345 346 347 352 353 354	<21: <22: <22: <22: <22: <22: <22: <22:	3 > OH 0 > FI 3 > OT 0 > FI 1 > NA 2 > LO 3 > OT 0 > 5 atg 9 Met A	RGANI CHER CATUI CATI CHER GCt (ISM: RE: INFO RE: INFO INFO Gag G	CDS (3). ORMAT	rion. (73 rion: cag c	scH 34)	gtg g	gag t	cct g	Gly (10	The the sequence of the sequen	types Seque tence ggc t	of ence I s for s ttg a Leu :	rrors s listing similar atc (Ile (bown e: . Please r errors. cag	cist thro check s	subsequent 17
340 342 343 345 346 346 352 352 353	<21: <22: <22: <22: <22: <22: <22: <22:	3 > OH 0 > FI 3 > O' 0 > FI 1 > NA 2 > LO 3 > O' 0 > 5 atg of Met A	RGANI PHER EATUR AME/I PCATI PHER GCt Q Ala (ISM: RE: INFO RE: ION: INFO Gag G	CDS (3). CDS (3). CRMAT	Cag colors	scH 34) ctg c	gtg gtal (gag t	cct g Ser (Gly (10 gcc	The the sequence of the sequen	types Seque tence ggc t Gly I	s of ence I s for s ttg a Leu I	rors s isting similar atc (Ile (acc	hown ender the second s	cist thro check s	subsequent
340 342 343 345 346 352 352 353 354 356	<21: <22: <22: <22: <22: <22: <22: <22:	3 > OH 0 > FI 3 > O' 0 > FI 1 > NA 2 > LO 3 > O' 0 > 5 atg of Met A	RGANI PHER EATUR AME/I PCATI PHER GCt Q Ala (ISM: RE: INFO RE: ION: INFO Gag G	CDS (3). CRMAT ORMAT Gtg (4) ctg Leu	Cag colors	scH 34) ctg c	gtg gtal (gag t	Ser (Gly (10 gcc	The the sequence of the sequen	types Seque tence ggc t Gly I	s of ence I s for s ttg a Leu I	rors s isting similar atc o Ile (acc Thr	hown ender the second s	cist thro check s	subsequent 17
340 343 345 346 347 351 352 353 354 356 356	<21: <22: <22: <22: <22: <22: <22: <20: cc i	3 > OI 3 > O' 3 > O' 5 > FI 1 > NI 2 > LO 3 > O' 0 > 5 atg of Met I 999 Gly	RGAN: CHER CHER CHER CHER GCT GCT GGT GGT GGT GGT GGT GGT GGT GGT	ISM: RE: INFO RE: INFO INFO Gag Q TCC Ser	CDS (3). ORMAT gtg (/al (ctg Leu 20	Cag of the state o	scl 34) ctg c Leu V	gtg g 7al (gag to state to the control of the state control of the state control of the control of the state of the stat	gca Ala	Gly (10 gcc Ala	The the sequence of the sequen	types Seque tence ggc t gga gga Gly	of ence I s for s ttg a Leu I ttc Phe	atc of the control of	bown er. Please rerrors. cag Sin ttc Phe	rist throcheck s	subsequent 17
340 343 345 346 346 351 352 354 356 356 356	<21: <22: <22: <22: <22: <22: <22: <20: <27: <27: <27: <27: <27: <27: <27: <27	3 > OI 3 > OI 3 > OI 5 > FI 1 > NI 2 > LO 3 > OI 0 > 5 atg of Met I 999 Gly	RGAN: CATURE CHER CATURE CHER CHER CHER CHER CHER CHER CHER CH	ISM: RE: INFO RE: INFO INFO Gag Glu tcc Ser cct	CDS (3). DRMAT gtg (7al (ctg Leu 20 atg	Cag of aga Arg	scl 34) ctg c ctc Leu	gtg g 7al (gag to state Cys	gca Ala 25	Gly (10 gcc Ala gcg	The the sequence of the sequen	types Seque tence ggc t gga gga Gly gga	ttg a Leu :	atc of the Control of	bown ender Please rerrors. cag Sin ttc Phe ctg	rist throcheck s	subsequent 17
340 343 345 346 347 352 353 354 356 356 360 360	<21: <22: <22: <22: <22: <22: <22: <20: cc ; cct Pro agc Ser	3 > OI 3 > OI 3 > OI 5 > FI 1 > NI 2 > LO 3 > OI 0 > 5 atg of Met I 999 Gly	RGAN: CATURE CHER CATURE CHER CHER CHER CHER CHER CHER CHER CH	ISM: RE: INFO RE: INFO INFO Slu tcc Ser cct Pro	CDS (3). DRMAT gtg (7al (ctg Leu 20 atg	Cag of aga Arg	scl 34) ctg c ctc Leu	gtg g 7al (gag telu state Cys	gca Ala 25	Gly (10 gcc Ala gcg	The the sequence of the sequen	types Seque tence ggc t gga gga Gly gga	ttg a Leu : ttc Phe aag	atc of the Control of	bown ender Please rerrors. cag Sin ttc Phe ctg	rist throcheck s	subsequent 17
340 343 345 346 347 352 353 354 356 356 363 363	<21: <22: <22: <22: <22: <22: <22: <20: cc i : cct Pro agc Ser	3 > OI 0 > FI 3 > O' 0 > FI 1 > NA 2 > LO 3 > O' 0 > 5 atg of Met A 1 ggg Gly ggc Gly	RGAN: EATUR THER EATUR AME/I DCAT: THER GCt G Ala G GGly tac Tyr	ISM: RE: INFO RE: INFO INFO Slu tcc Ser cct Pro 35	CDS (3) CRMAT Gtg (4) Ctg Leu 20 atg Met	Cag of aga arg	scl 34) ctg g ctc Leu tgg	gtg g /al (tcc Ser gtc Val	gag to state to the control of the c	Ser (gca Ala 25 cag	Gly (10 gcc Ala gcg Ala	The the sequence of the sequen	types Seque tence ggc t gga Gly ggg Gly	ttg a Leu : ttc Phe aag Lys 45	atc of the Control of	bown es. Please rerrors. cag Sin ttc Phe ctg Leu	rist throcheck s	subsequent 17 95
340 343 345 345 346 352 353 354 356 356 366 366	<21: <220 <22: <22: <22: <22: <22: <400 cc a cct Pro agc Ser gag	3 > OI 3 > OI 3 > OI 5 > FI 1 > NA 2 > LO 3 > OI 0 > 5 atg of Met A 1 ggg Gly ggc Gly tgg	RGAN: EATUR THER EATUR AME/I CCAT: THER GCt G Ala G GGly tac Tyr gtg	ISM: RE: INFO RE: INFO REY: INFO Slu tcc Ser cct Pro 35 gca	CDS (3) CRMAT Gtg (4) Ctg Leu 20 atg Met	Cag of aga Arg aac Asn ata	scl 34) ctg g ctc Leu tgg Trp	gtg g /al (tcc Ser gtc Val	gag to state to the control of the c	gca Ala 25 cag Gln	Gly (10 gcc Ala gcg Ala agt	The the sequence of the sequen	types Seque tence ggc t sly I gga Gly ggg Gly aaa	ttg a Leu : ttc Phe aag Lys 45	atc of the Control of	bown es. Please rerrors. cag Sin 15 ttc Phe ctg Leu gca	rist throcheck s	subsequent 17
340 343 345 346 347 352 352 353 354 356 361 362 364	<21: <220 <22: <22: <22: <22: <400 cc a cct Pro agc ser gag Glu	3 > OI 3 > OI 3 > OI 5 > FI 1 > NI 2 > LO 3 > OI 0 > 5 atg of Met I 1 ggg Gly ggc Gly	RGAN: EATUR THER EATUR AME/I CCAT: THER Ala (GG1y tac Tyr gtg Val	ISM: RE: INFO RE: INFO REY: INFO Slu tcc Ser cct Pro 35 gca	CDS (3) CRMAT Gtg (4) Ctg Leu 20 atg Met	Cag of aga Arg aac Asn ata	scl 34) ctg g ctc Leu tgg Trp	tcc Ser gtc Val	gag to state to the control of the c	gca Ala 25 cag Gln	Gly (10 gcc Ala gcg Ala agt	The the sequence of the sequen	types Seque tence ggc t gga Gly ggg Gly aaa Lys	ttg a Leu : ttc Phe aag Lys 45	atc of the Control of	bown es. Please rerrors. cag Sin 15 ttc Phe ctg Leu gca	rist throcheck s	subsequent 17 95
340 343 345 346 347 352 352 353 356 360 360 360 360	<21: <220 <22: <22: <22: <22: <400 cc a cct Pro agc Ser gag Glu	3 > OI 0 > FI 3 > O' 0 > FI 1 > NX 2 > LO 3 > O' 0 > 5 atg 9 atg 9 Gly tgg Trp	RGAN: EATUR THER EATUR AME/I CCAT: THER Ala (GGly tac Tyr gtg Val 50	ISM: RE: INFO RE: CEY: INFO Sag of Cot Ser Cot Pro 35 Gca Ala	CDS (3) CRMAT Gtg (4) Ctg Leu 20 atg Met gtt Val	Cag of Arg aac Asn ata	scI 34) ctg s ctc Leu tgg Trp tca Ser	tcc Ser gtc Val tat Tyr 55	gag to state the control of the cont	gca Ala 25 cag Gln gga Gly	Gly (10 gcc Ala gcg Ala agt Ser	The the sequence of the sequence of the ser	types Seque tence ggc t sly I gga Gly ggg Gly aaa Lys 60	ttg a ttc phe aag Lys 45 tac	atc of the control of	hown es. Please rerrors. cag Sin ttc Phe ctg Leu gca Ala	cist throcheck s	subsequent 47 95 43
340 343 345 346 347 352 352 353 354 356 366 366 366	<21: <220 <22: <22: <22: <22: <400 cc a cct Pro agc Ser gag Glu gac	3 > OI 0 > FI 3 > O' 0 > FI 1 > NX 2 > LO 3 > O' 0 > 5 atg 9 Met X 1 ggg Gly ggc Gly tgg Trp	RGAN: EATUR THER EATUR AME/I CCAT: THER Ala (GGly tac Tyr gtg Val 50 gtg	ISM: RE: INFO RE: INFO RE: INFO RES INFO RES	CDS (3) CRMAT Gtg (4) Ctg Leu 20 atg Met gtt Val	Cag of aga Arg aac Asn ata Ile	scI 34) ctg s ceu v ctc Leu tgg Trp tca ser	tcc Ser gtc Val tat Tyr 55 acc	gag to state of the state of th	gca Ala 25 cag Gln gga Gly	Gly (10 gcc Ala gcg Ala agt Ser aga	The the sequence of the sequen	Types Seque tence ggc t Gly I gga Gly aaa Lys 60 aat	ttg a ttc Phe aag Lys 45 tac Tyr	atc of the control of	hown es. Please rerrors. cag Sin 15 ttc Phe ctg Leu gca Ala aac	cist throcheck s	subsequent 17 95
340 343 343 345 346 351 352 353 354 356 366 366 366 366 366	<21: <22: <22: <22: <22: <22: <400 cc i cct Pro agc Ser gag Glu gac Asp	3 > OI 3 > OI 3 > OI 5 > FI 1 > NI 2 > LO 3 > OI 0 > 5 atg of 1 ggg Gly tgg Trp tcc Ser	RGAN: EATUR THER EATUR AME/I CCAT: THER Ala (GGly tac Tyr gtg Val 50 gtg	ISM: RE: INFO RE: INFO RE: INFO RES INFO RES	CDS (3) CRMAT Gtg (4) Ctg Leu 20 atg Met gtt Val	Cag of aga Arg aac Asn ata Ile	scl 34) ctg s ctc Leu tgg Trp tca Ser ttc	tcc Ser gtc Val tat Tyr 55 acc	gag to state of the state of th	gca Ala 25 cag Gln gga Gly	Gly (10 gcc Ala gcg Ala agt Ser aga	The the sequence of the sequen	Types Seque tence ggc t Gly I gga Gly aaa Lys 60 aat	ttg a ttc Phe aag Lys 45 tac Tyr	atc of the control of	hown es. Please rerrors. cag Sin 15 ttc Phe ctg Leu gca Ala aac	cist throcheck s	subsequent 47 95 43
340 343 343 345 346 351 352 353 354 356 366 366 366 366 366 366 366 366 366	<21: <22: <22: <22: <22: <22: <20: <20: cct Pro agc Ser gag Glu gac Asp	3 > OI 3 > OI 3 > OI 3 > OI 1 > NA 2 > LO 3 > OI 0 > 5 atg of 1 ggg Gly tgg Trp tcc ser 65	RGAN: CHER CHER CHER CHER CHER CHER CHER CHER	ISM: RE: INFO RE: INFO REY: INFO REGULA CCC Ser CCC Pro 35 GCa Ala aag Lys	CDS (3) CRMAT Gtg (7) Ctg Leu 20 atg Met Val gtt Val	cag of the second secon	scient start	tcc Ser gtc Val tat Tyr 55 acc Thr	gag to state the control of the cont	gca Ala 25 Cag Gln gga Gly tcc Ser	Gly (10 gcc Ala gcg Ala agt Ser aga Arg	The the sequence of the sequen	types Seque tence ggc t Gly I gga Gly aaa Lys 60 aat Asn	ttg a Leu : ttc Phe aag Lys 45 tac Tyr tcc Ser	atc of the contract of the con	hown es. Please rerrors. cag Sin 15 ttc Phe ctg Leu gca Ala aac Asn	rist throcheck s	subsequent 47 95 43 91
340 343 343 345 346 351 352 353 354 356 366 366 366 366 366 366 366 366 366	<21: <22: <22: <22: <22: <22: <400 cc i cct Pro agc Ser gag Glu gac Asp	3 > OI 3 > OI 3 > OI 3 > OI 1 > NA 2 > LO 3 > OI 0 > 5 atg of 1 ggg Gly tgg Trp tcc ser 65	RGAN: CHER CHER CHER CHER CHER CHER CHER CHER	ISM: RE: INFO RE: INFO REY: INFO REGULA CCC Ser CCC Pro 35 GCa Ala aag Lys	CDS (3) CRMAT Gtg (7) Ctg Leu 20 atg Met Val gtt Val	cag of the second secon	scient start	tcc Ser gtc Val tat Tyr 55 acc Thr	gag to state the control of the cont	gca Ala 25 Cag Gln gga Gly tcc Ser	Gly (10 gcc Ala gcg Ala agt Ser aga Arg	The the sequence of the sequen	types Seque tence ggc t Gly I gga Gly aaa Lys 60 aat Asn	ttg a Leu : ttc Phe aag Lys 45 tac Tyr tcc Ser	atc of the contract of the con	hown es. Please rerrors. cag Sin 15 ttc Phe ctg Leu gca Ala aac Asn	rist throcheck s	subsequent 47 95 43

VERIFICATION SUMMARYDATE: 12/28/2004PATENT APPLICATION: US/10/517,941TIME: 11:51:27

Input Set : D:\0077 (OX40).ST25.txt
Output Set: N:\CRF4\12282004\J517941.raw

L:12 M:270 C: Current Application Number differs, Replaced Current Application No L:12 M:271 C: Current Filing Date differs, Replaced Current Filing Date L:33 M:258 W: Mandatory Feature missing, <223> Blank for SEQ#:1,Line#:30 L:189 M:258 W: Mandatory Feature missing, <223> Blank for SEQ#:3,Line#:186 L:351 M:258 W: Mandatory Feature missing, <223> Blank for SEQ#:5,Line#:348 L:505 M:258 W: Mandatory Feature missing, <223> Blank for SEQ#:7,Line#:502 L:659 M:258 W: Mandatory Feature missing, <223> Blank for SEQ#:9,Line#:656 L:813 M:258 W: Mandatory Feature missing, <223> Blank for SEQ#:11,Line#:810 L:969 M:258 W: Mandatory Feature missing, <223> Blank for SEQ#:13,Line#:966 L:1123 M:258 W: Mandatory Feature missing, <223> Blank for SEQ#:15,Line#:1120 L:2157 M:258 W: Mandatory Feature missing, <223> Blank for SEQ#:33,Line#:2154 L:2199 M:258 W: Mandatory Feature missing, <223> Blank for SEQ#:35,Line#:2196 L:2241 M:258 W: Mandatory Feature missing, <223> Blank for SEQ#:37,Line#:2196